

Morteza Sabri

+49 15510595621 | morteza_sabri@icloud.com | 52066 Aachen, Germany

[Portfolio](#) | [LinkedIn](#) | [Github](#) | [GoogleScholar](#) | [Orcid](#)

PROFESSIONAL SUMMARY

Experienced bioinformatician specializing in bulk and single-cell RNA-Seq analysis—applied to cardiovascular and neurodevelopment research—proficient in R, Shell, and HPC. Developed pipelines accelerating analysis by 80%, identifying novel biomarkers, boosting productivity and reproducibility. Passionate about teaching and solving biological problems through bioinformatics. For more about my background and selected projects, please see my portfolio: <https://mortezasabri.github.io/>

HIGHLIGHTED AREAS OF EXPERTISE

- Bulk & single-cell RNA-Seq
- Data Visualization & Reproducibility
- R programming & Shell Scripting
- Study design & Data Interpretation

EXPERIENCE

Scientific Staff, Bioinformatician | RWTH Aachen University, Aachen Jan 2025 – Apr 2025

- Performed single-cell RNA-Seq analysis to study neuron migration in the absence of DNMT1.
- Conducted methylation array data analysis on 64 subjects with postpartum depression.
- Handled data preprocessing (Parse Bioscience's Trailmaker), statistical analysis, and visualization (R).

Scientific Staff, Bioinformatician | Technical University of Munich, Munich Nov 2023 - Nov 2024

- Conducted bulk and single-cell RNA-Seq analyses for cardiovascular research.
- Managed workflows from raw data to functional interpretation and identifying new biomarkers.
- Generated publication-ready visualizations illustrating gene-disease associations.
- Optimized preprocessing pipelines with R/Shell scripting, reducing runtime up to 80%.

Guest Scientist, Bioinformatician | Helmholtz Munich, Munich Oct 2024 - Nov 2024

- Performed deconvolution analysis to interpret bulk RNA-Seq datasets using BayesPrism R package to elucidate cell-type composition.

Instructor & Freelance, Bioinformatician | Self-Employed, Tehran 2019 – 2022

- Delivered over 10 onsite workshops on R programming, RNA-Seq, and Linux/Shell scripting.
- Provided freelance bioinformatics services including RNA-Seq, epigenomics, and visualization.
- Supported manuscript revisions by performing advanced statistical analyses (e.g., MINT).
- Hosted Biocast101 podcast ([Apple](#), [Spotify](#), [Castbox](#), [PodLink](#)).
- Created contents on social media known as Bioinformatics101 ([YouTube](#), [Instagram](#), etc).

SKILLS

Laboratory Techniques:

- RNA/DNA extraction
- PCR & qRT-PCR
- Primer design

Programming Languages:

- R
- Shell/Bash
- Markdown & LaTeX
- Git & GitHub
- MATLAB (basic)
- Python (basic)

Bioinformatics Workflows:

- Bulk & single-cell RNA-seq
- ChIP-Seq

- Genome Assembly
- Expression & Methylation Arrays

Software and HPC:

- CLC Genomics Workbench
- Galaxy
- Jupyter Notebooks
- SPSS
- Sherlock & RWTH Aachen cluster

Transferable & Soft Skills

- Paper writing
- Teaching & Mentoring: tutorials or workshops
- Open Science & Reproducibility
- FAIR data principles & metadata standards
- Teamwork & communication

EDUCATION

M.Sc. Biology (Genetics), University of Sistan and Baluchestan, Iran

- **Thesis:** "Investigation of Superoxide Dismutase and Catalase Gene Expression under Drought Stress: A Comparative Study between Sistan and Baluchestan and Moderate Cultivars".

B.Sc. Cellular and Molecular Biology (Genetics), Islamic Azad University, Iran

CERTIFICATIONS & LANGUAGES

TOEFL iBT, ETS - Score: 110, February 2023

Languages: Persian (Native), English (Proficient), Azeri (Basic)

PUBLICATION

Overcoming trastuzumab resistance in HER2-positive breast cancer, Journal of Cellular Physiology, 2019.

[DOI: 10.1002/jcp.29216](https://doi.org/10.1002/jcp.29216)

Evaluation of monolignol biosynthesis gene network in Camelina sativa, Agricultural Biotechnology Journal, 2020.

Investigation of Superoxide Dismutase and Catalase Gene Expression under Drought Stress: A Comparative Study between Sistan and Baluchestan and Moderate Cultivars – (Draft)

TEACHING EXPERIENCE

Workshops: R & Linux/Shell programming, RNA-Seq, Visualization and basic stats in R

[Certificates and materials on my portfolio](#)

HIGHLIGHTED PIPELINES

- Bulk RNA-Seq (STAR/HISAT2 → DESeq2/edgeR → GO/KEGG)
- scRNA-Seq (Seurat & SingleCellExperiment)
- Genome assembly (Velvet, SPAdes)
- Epigenomic analyses (limma on IDAT files)

[More details on my portfolio](#)

INTERESTS

Genome editing, Machine learning, Comparative genomics, Data science, Computer science

Climbing, Hiking, Camping, Mountaineering

REFERENCE

Prof. Dr. Lars Mägddefessel

Dr. Mahboubeh Yazdanifar

Dr. Komeil Razmi

lars.maegdefessel@tum.de

maribel.yazdanifar@myome.com

komeil.razmi@csiro.au